This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (Currently Amended) A method of correlating gene and protein expression in a biological sample, the method comprising the steps of:

a) obtaining the biological sample;

b) generating a gene expression profile of the sample, thereby identifying an mRNA expressed in the sample;

c) identifying ~~a~~ one or more physio-chemical ~~property~~ properties of a polypeptide encoded by the mRNA by determining the amino acid sequence of the polypeptide encoded by the mRNA, wherein the physiochemical property is selected from the group consisting of molecular weight, iso-electric point, hydrophobicity, hydrophilicity, glycosylation, phosphorylation, epitope sequence, ligand binding sequence, charge at a specified pH, and metal chelate binding;

d) fractionating polypeptides in the sample on the basis of the one or more physio-chemical properties ~~property and~~;

e) ~~identifying the polypeptide encoded by the mRNA from among the fractionated proteins, wherein the identified polypeptide comprises the physio-chemical property~~ selecting one or more candidate polypeptides from among the fractionated polypeptides, which candidate polypeptides comprises the physio-chemical property;

f) determining the identity of the one or more candidate polypeptides and

g) correlating the identity of the candidate polypeptide or polypeptides with the polypeptide encoded by the mRNA; thereby correlating gene and protein expression in the sample.

2. (As filed) The method of claim 1, wherein the biological sample comprises a cell lysate from a healthy cell.

3. (As filed) The method of claim 1, wherein the biological sample comprises a cell lysate from a pathological cell.

4. (As filed) The method of claim 1, wherein the biological sample comprises a cell lysate from a cell contacted by a toxic compound.

5. (Currently Amended) The method of claim 1, wherein the biological sample comprises a cell lysate from a cell of a subject who ~~respond~~ responds to a drug treatment or a subject who does not respond to a drug treatment.

6. (As filed) The method of claim 1, wherein the biological sample comprises a cell lysate from a cell exposed to heat, cold, or radiation.

7. (As filed) The method of claim 1, wherein the biological sample comprises a human cell.

8. (As filed) The method of claim 1, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with an EST array.

9. (As filed) The method of claim 1, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with an oligonucleotide array.

10. (As filed) The method of claim 1, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with an mRNA array.

11. (As filed) The method of claim 1, wherein the mRNA is differentially expressed in two biological samples.

12. (As filed) The method of claim 11, wherein the two biological samples are derived from a normal cell and a pathologic cell.

13. (As filed) The method of claim 12, wherein the pathologic cell is a cancer cell.

14. (As filed) The method of claim 11, wherein the two biological samples are derived from a healthy cell and a cell exposed to a toxic compound.

15. (Currently Amended) The method of claim 1, wherein the step of identifying the one or more physio-chemical ~~property~~ properties of the polypeptide encoded by the mRNA further comprises identifying a plurality of physio-chemical properties.

16. (Currently Amended) The method of claim 1, wherein the step of identifying ~~a~~ the one or more physio-chemical ~~property~~ properties comprises predicting the masses of proteolytic fragments generated by the polypeptide encoded by the mRNA upon degradation of the polypeptide by a selected proteolytic agent, and the step of determining the identity of the one or more candidate polypeptides ~~identifying the polypeptide encoded by the mRNA~~

comprises subjecting polypeptides in the sample to degradation by the agent and identifying actual proteolytic fragments in the sample having masses that correspond to the masses of the predicted fragments.

17. (Canceled)

18. (As filed) The method of claim 1, wherein the step of fractionating the polypeptides in the sample comprises 2D-gel electrophoresis.

19. (As filed) The method of claim 1, wherein the step of fractionating the polypeptides in the sample comprises mass spectrometry.

20. (Currently amended) The method of claim ~~1~~ 19, wherein the step of fractionating the polypeptides in the sample comprises surface enhanced laser desorption ionization, wherein the surface enhanced laser desorption ionization comprises fractionating by affinity retention on solid phase-bound adsorbent followed by fractionating retained polypeptides from the solid phase by ~~gas-phase ion~~ mass spectrometry.

21. (Canceled)

22. (Canceled)

23. (Canceled)

24. (Currently Amended) The method of claim 1, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with ~~an EST~~ a nucleic acid array.

25. (Currently Amended) The method of claim 1, wherein the step of generating the gene expression profile comprises identifying expressed mRNA with ~~an oligonucleotide array~~ a northern blot or a dot blot.

26. (Canceled)

27. (Canceled)

28. (Canceled)

29. (Canceled)

30. (Canceled)

31. (New) The method of claim 1 wherein fractionating the polypeptides comprises chromatography.

32. (New) The method of claim 1 wherein fractionating the polypeptides comprises chromatography followed by mass spectrometry.

33. (New) The method of claim 32 wherein mass spectrometry is laser desorption/ionization mass spectrometry.

34. (New) The method of claim 32 wherein mass spectrometry is SELDI.

35. (New) The method of claim 31 wherein chromatography comprises ion exchange chromatography.

36. (New) The method of claim 32 wherein chromatography comprises ion exchange chromatography.

37. (New) The method of claim 20 wherein the solid phase bound adsorbent is selected from an ion exchange adsorbent, a hydrophilic adsorbent, a hydrophobic adsorbent and a metal chelate adsorbent.

38. (New) The method of claim 20 wherein the solid phase bound adsorbent is a biospecific affinity adsorbent.

39. (New) The method of claim 38 wherein the biospecific affinity adsorbent comprises an antibody.

40. (New) The method of claim 15, wherein the step of fractionating the polypeptides in the sample comprises mass spectrometry.

41. (New) The method of claim 40, wherein the step of fractionating the polypeptides in the sample comprises surface enhanced laser desorption ionization, wherein the surface enhanced laser desorption ionization comprises fractionating by affinity retention on solid phase-bound adsorbent followed by fractionating retained polypeptides from the solid phase by mass spectrometry.

42. (New) The method of claim 41 wherein the solid phase bound adsorbent is selected from an ion exchange adsorbent, a hydrophilic adsorbent, a hydrophobic adsorbent and a metal chelate adsorbent.

43. (New) The method of claim 41 wherein the solid phase bound adsorbent is a biospecific affinity adsorbent.

44. (New) The method of claim 43 wherein the biospecific affinity adsorbent comprises an antibody.

45. (New) The method of claim 24, wherein the step of fractionating the polypeptides in the sample comprises mass spectrometry.

46. (New) The method of claim 45, wherein the step of fractionating the polypeptides in the sample comprises surface enhanced laser desorption ionization, wherein the surface enhanced laser desorption ionization comprises fractionating by affinity retention on solid phase-bound adsorbent followed by fractionating retained polypeptides from the solid phase by mass spectrometry.

47. (New) The method of claim 46 wherein the solid phase bound adsorbent is selected from an ion exchange adsorbent, a hydrophilic adsorbent, a hydrophobic adsorbent and a metal chelate adsorbent.

48. (New) The method of claim 46 wherein the solid phase bound adsorbent is a biospecific affinity adsorbent.

49. (New) The method of claim 48 wherein the biospecific affinity adsorbent comprises an antibody.

50. (New) The method of claim 20 wherein the solid phase bound adsorbent is selected from an ion exchange adsorbent, a hydrophilic adsorbent, a hydrophobic adsorbent and a metal chelate adsorbent.

51. (New) The method of claim 50 wherein the solid phase bound adsorbent is a biospecific affinity adsorbent.

52. (New) The method of claim 51 wherein the biospecific affinity adsorbent comprises an antibody.

53. (New) The method of claim 1 wherein fractionating the polypeptides comprises affinity chromatography followed by mass spectrometry.

54. (New) The method of claim 1, comprising the step of removing post translational modifications of polypeptides prior to the fractionation of step (d).